

Supplemental Information

Fig. S1. Multi-angle light scattering analysis of Nup358^{CTD}. The differential refractive index and determined molecular weight are plotted against elution volume off of a Superdex 75 10/300 GL gel-filtration column.

Fig. S2. Multi-species sequence alignment of Nup358^{CTD}. The overall sequence identity is shaded from white (less than 60 % identity) to red (100 % identity). The secondary structure as observed in the Nup358^{CTD} structure is shown above the alignment, with blue bars representing α helices and green arrows representing β strands. The sequence of human cyclophilin A is displayed at the bottom of the alignment with residues identical to human Nup358^{CTD} shaded in grey. Gray and magenta dots indicate identical and different active site residues between human Nup358^{CTD} and human cyclophilin A, respectively. The numbering below the sequence is relative to human Nup358.

Fig. S3. Isothermal titration calorimetry (ITC) analysis. Upper parts of each box show raw data and lower parts show integrated heat changes corrected for heat from dilution for interactions between (a) Nup358^{CTD} and HIV-1^{CA} and (b) Nup358^{CTD} V3173W and HIV-1^{CA}.

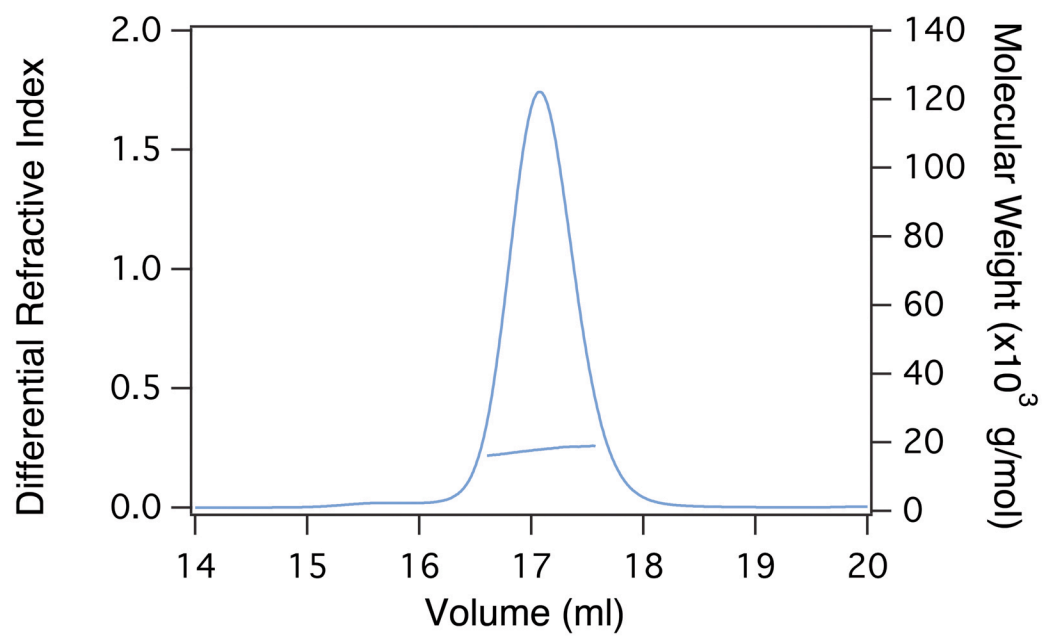


Figure S1, Lin et al., 2012

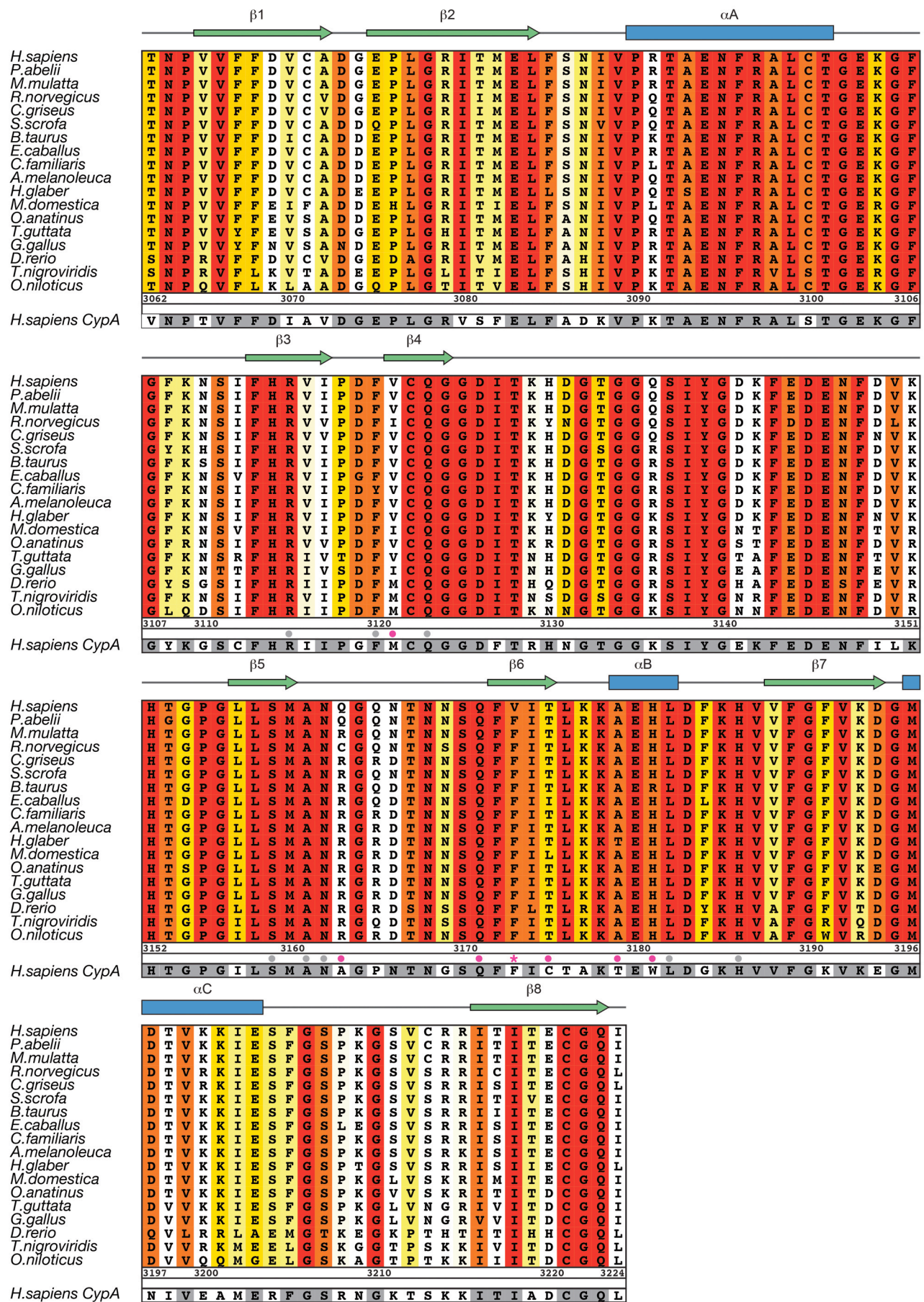
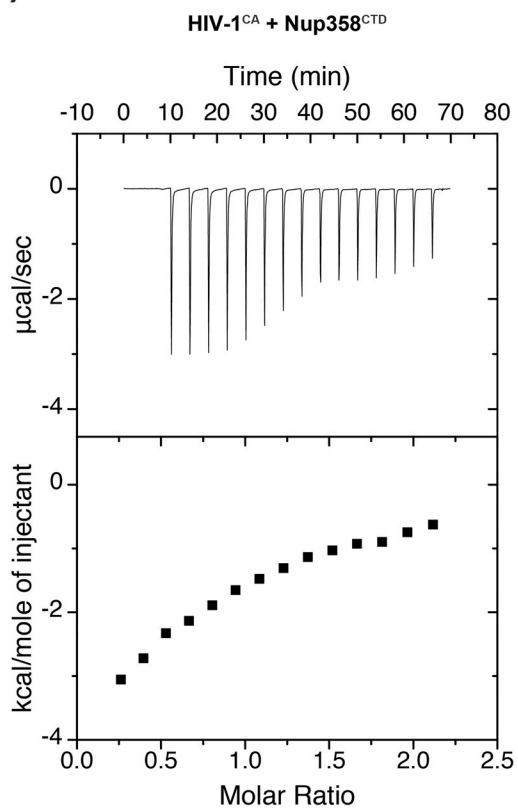


Figure S2, Lin et al., 2012

(a)



(b)

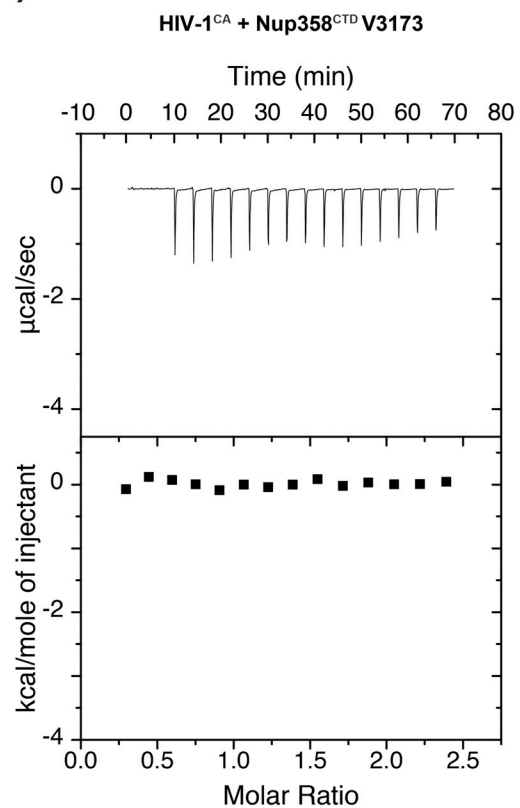


Figure S3, Lin et al., 2012